

TITLE: USE OF SILVER GENE FOR THE AUTHENTICATION OF THE RACIAL ORIGIN OF ANIMAL POPULATIONS, AND OF THE DERIVATIVE PRODUCTS THEREOF

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		5' UTR	
SIL5	-29	GGTCTTTGGTTGCTGGAAGGAAGAACAGG	10
	1	ATG GAT CTG GTG CTG AGA AAA TAC CTT CTC	30
		M D L V L R K Y L L	
H V A L M G V L L A V R T T E G P R	28		
CAT GTG GCT CTG ATG GGT GTT CTT CTG GCT GTA AGG ACC ACA GAA GGA CCC AGA	84		
D R D W L G V S R Q L R I K A W N R	46		
GAC AGG GAC TGG CTT GGT GTC TCA AGG CAG CTC AGA ATT AAA GCA TGG AAC AGA	138		
Q L Y P E W T E S Q G P D C W R G G	64		
CAG CTG TAT CCA GAG TGG ACA GAA AGC CAG GGG CCT GAC TGC TGG AGA GGT GGC	192		
H I S L K V S N D G P T L I G A N A	82		
CAC ATA TCC CTG AAG GTC AGC AAT GAT GGG CCT ACA CTG ATT GGG GCA AAT GCT	246		
S F S I A L H		← SIL2	
TCC TTC TCT ATT GCC TTG CAC TTT CCT AAA AGC CAA AAG GTG CTG CCA GAT GGG	100		
	300		
Q V I W A N N T I I N G S Q V W G G	118		
CAG GTC ATC TGG GCC AAC AAC ACC ATC ATC AAT GGG AGC CAG GTG TGG GGA GGA	354		
Q L V Y P Q E		← SIL1	
CAG CTG GTA TAT CCC CAA GAA CCT GAT GAT ACC TGC ATC TTC CCC GAT GGG GAG	136		
	408		
P C P S G P L S Q K R C F V Y V W K	154		
CCC TGC CCT TCT GGC CCT CTA TCT CAG AAA AGA TGC TTT GTT TAT GTC TGG AAG	462		
T W D Q Y W Q V L G G P V S G L S I	172		
ACC TGG GAC CAA TAC TGG CAA GTT CTG GGG GGC CCA GTG TCT GGA CTG AGC ATC	516		
G T D K A M L G T Y N M E V T V Y H	190		
GGG ACA GAC AAG GCA ATG CTG GGC ACA TAT AAC ATG GAA GTG ACT GTC TAC CAC	570		
R R G S Q S Y V P L A H S S S A F T	208		
CGC CGG GGG TCC CAG AGC TAT GTG CCC CTC GCT CAC TCC AGT TCA GCC TTC ACC	624		
I T D Q V P F S V S V S Q L Q A L D	226		
ATT ACT GAC CAG GTG CCC TTC TCT GTG AGT GTG TCT CAG CTG CAG GCC TTG GAT	678		
G R N K R F L R K Q P L T F A L Q L	244		
GGA AGG AAC AAG CGC TTC CTG AGA AAG CAG CCT CTG ACC TTT GCC CTC CAG CTC	732		
H D P S G Y L A G A D L S Y T W D F	262		
CAT GAT CCC AGT GGC TAT TTG GCT GGG GCT GAC CTT TCC TAC ACC TGG GAC TTT	786		
G D S T G T L I S R A L T V T H T Y	280		
GGT GAC AGT ACA GGG ACC CTG ATC TCT CGG GCA CTC ACG GTC ACT CAC ACT TAC	840		
L E S G P V T A Q V V L Q A A I P L	298		
CTA GAG TCT GGC CCA GTC ACT GCA CAG GTG GTG CTG CAG GCT GCC ATT CCT CTC	894		
T S C G S S P V P G T T D R H V T T	316		
ACC TCC TGT GGC TCC TCT CCA GTT CCA GGC ACT ACA GAT AGG CAT GTG ACA ACT	948		
A E A P G T T A G Q V P T T E V M G	334		
GCA GAG GCT CCT GGA ACC ACA GCT GGC CAA GTG CCT ACT ACA GAA GTC ATG GGC	1002		
T T P G Q V P T A E A P G T T V G W	352		
ACC ACA CCT GGC CAG GTG CCA ACT GCA GAG GCC CCT GGC ACC ACA GTT GGG TGG	1056		
V P T T E D V G T T P E Q V A T S K	370		
GTG CCA ACC ACA GAG GAT GTA GGT ACC ACA CCT GAG CAG GTG GCA ACC TCC AAA	1110		
V L S T T P V E M P T A K A T G R T	388		
GTC TTA AGT ACA ACA CCA GTG GAG ATG CCA ACT GCA AAA GCT ACA GGT AGG ACA	1164		

Figure 1

TITLE: USE OF SILVER GENE FOR THE AUTHENTICATION OF THE RACIAL ORIGIN OF ANIMAL POPULATIONS, AND OF THE DERIVATIVE PRODUCTS THEREOF

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P	E	V	S	T	T	E	P	S	G	T	T	V	T	Q	G	T	T	406	
CCT	GAA	GTG	TCA	ACT	ACA	GAG	CCC	TCT	GGA	ACC	ACA	GTT	ACA	CAG	GGA	ACA	ACT	1218	
P	E	L	V	E	T	T	A	G	E	V	S	T	P	E	P	A	G	424	
CCA	GAG	CTG	GTG	GAG	ACC	ACA	GCT	GGA	GAG	GTG	TCC	ACT	CCT	GAG	CCT	GCG	GGT	1272	
S	N	T	S	S	F	M	P	T	E	G	T	A	G	S	L	S	P	442	
TCA	AAT	ACT	AGC	TCA	TTC	ATG	CCT	ACA	GAA	GGT	ACT	GCA	GGC	TCC	CTG	AGT	CCC	1326	
L	P	D	D	T	A	T	L	V	L	E	K	R	Q	A	P	L	D	460	
CTG	CCG	GAT	GAC	ACT	GCC	ACC	TTA	GTC	CTG	GAG	AAG	CGC	CAA	GCC	CCC	CTG	GAT	1380	
C	V	L	Y	R	Y	G	S	F	S	L	T	L	D	I	V	Q	G	478	
TGT	GTT	CTG	TAT	CGC	TAT	GGC	TCC	TTT	TCC	CTC	ACC	CTG	GAC	ATT	GTC	CAG	GGT	1434	
I	E	S	A	E	I	L	Q	A	V	S	S	S	E	G	D	A	F	496	
ATT	GAG	AGT	GCT	GAG	ATC	CTA	CAG	GCT	GTG	TCA	TCC	AGT	GAA	GGA	GAT	GCA	TTT	1488	
E	L	T	V	S	C	Q	G	G	L	P	K	E	A	C	M	D	I	514	
GAG	CTG	ACT	GTG	TCT	TGC	CAA	GGC	GGG	CTA	CCC	AAG	GAA	GCC	TGC	ATG	GAC	ATC	1542	
S	S	P	G	C	Q	L	P	A	Q	R	L	C	Q	P	V	P	P	532	
TCA	TCG	CCA	GGG	TGT	CAG	CTG	CCT	GCC	CAG	CGG	CTG	TGT	CAG	CCT	GTG	CCC	CCC	1596	
S	P	A	C	Q	L	V	L	H	Q	V	L	K	G	G	S	G	T	550	
AGC	CCA	GCC	TGC	CAG	CTG	GTT	TTG	CAC	CAG	GTA	CTG	AAG	GGT	GGC	TCA	GGG	ACC	1650	
Y	C	L	N	V	S	L	A	D	A	N	S	L	A	M	V	S	T	568	
TAC	TGC	CTC	AAT	GTG	TCT	TTG	GCT	GAT	GCC	AAT	AGC	CTG	GCG	ATG	GTC	AGC	ACC	1704	
SIL3 →																			
Q	L	V	M	P	G	Q	E	A	G	L	R	Q	A	P	L	F	V	586	
CAG	CTT	GTC	ATG	CCT	GGG	CAA	GAA	GCA	GGC	CTC	AGG	CAG	GCT	CCT	CTG	TTC	GTG	1758	
G	I	L	L	V	L	T	A	L	L	L	A	S	L	I	Y	R	R	604	
GGC	ATC	TTG	CTG	GTG	CTA	ACA	GCT	TTG	TTG	CTT	GCA	TCT	CTG	ATA	TAC	AGG	CGA	1812	
R	L	M	K	Q	G	S	A	V	P	L	P	Q	L	P	H	G	R	622	
AGA	CTT	ATG	AAG	CAA	GGC	TCA	GCA	GTC	CCC	CTT	CCC	CAG	CTG	CCA	CAC	GGT	AGA	1866	
T	Q	W	L	R	L	P	W	V	F	R	S	C	P	I	G	E	S	640	
ACC	CAG	TGG	CTA	CGT	CTG	CCC	TGG	GTC	TTC	CGC	TCT	TGC	CCC	ATT	GGT	GAG	AGC	1920	
K	P	L	L	S	G	Q	Q	V	*	← SIL7								649	
AAA	CCC	CTC	CTC	AGT	GGA	CAG	CAG	GTC	TGA	GTG	CTC	TTA	TGT	GAA	GTC	ATG	ATT	1974	
SIL4 →																			
TAC	CCA	GGT	GGA	CAG	CAA	GGC	CTG	TCT	TTT	CTC	TGG	TCT	TCC	CTC	AGA	GAC	TAC	2028	
← SIL6																			
CAT	TGC	CTG	AAA	TAA	AGA	CTC	AGA	ACT	TG	SIL9								Poly(A)	2057
← 3'UTR																			

Figure 1 (continued)

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SIL10  
GTTGCTGGAAGGAAGAACAGGATGGATCTGGTGCTGAGAAAATACCTTCTCCATGTGGCTCTGATGGGTGTTCTTCTGGC 80  
TGTAAGGACCACAGAAGGTGAGTGTGGGATGTTGGACATGAACAAGTGTGAATTTGGGGTTGCACACCTGCTCTGGTTTT 160  
TCTCTCCCTAAATGGAAGATATCAGTAGTGCTTCAGGTGTCTCCCACCCATTGATTAGTGAGGACATGGGCAACTGA 240  
GCTCCCTCCCCACATGAAGATTTGGGTGCATGTGTGTTTCAGGCACTTGGGACTGAACCTGAAAACAACCCCATCTACCTG 320  
GATGGGTGAGAGAACAGTATGTCTCCGTGGCCCTAATTTTGAGATGCTCTGAATAGTGAGCTGGAACATGGGTGCCAAGG 400  
TAGTAAATGAGTGGAACCTCATTTAGGCTTTGTCTCAGGCACTTGGGATAGGGTATTTAGGAGATAGAGAAAGATAGGA 480  
GATAGGAGAAAGGAGAAAGAGGATGTGGTATTGGATAGAAGGGTAATGAGGCACCTCATCCCTCTTTGGGATGGGCATG 560  
GGTGAACACAGCCCAGGCTTTTGTCTGGGGCTGGAAGAGACAGGCAGAAGGGTCTCAGCTGAGCATCACATGAAAGGGC 640  
TCTGGGGGATTGGGGCCTCGTGACAGGAGCAAGGCGGGTGGGGTGGGGATGGTGAGAGGGTCTGGAATGTCCCGTGCTGC 720  
TCTGAGGAGGGAGGATTGGGAGTGGAGAAAGAATGGGGCATCTTATGATTCTCTTGTCTTGTGGTGAGGTATTCAGTGG 800  
GATAATCTAGATCCTCCCCAAGAGAATCAACCAGGTTTCTGGTACATGTTAGAGATGGAGTGAGGATAGTCTGTGATG 880  
TGCAGAAATATCTACATTGTACCCAGTGCCCCCTTTCTCTAGATCCCTGGTCTCACAGACTTCTTGGAACTTCTCCTTG 960  
ATCTGACTTCCCTCATTTCATGGTGTCAATTTCAAGTCTTATTCTTTTACTATGTTTCTGTTATTGTATTCTGGAATATCCTG 1040  
TTCATATGTGTCCACCAAGGCTCTTAATATGTTGTGCTTACTTTTTGGATCCAGATTTTTAAATCATAAGAAGACATT 1120  
TTTATATAGTTCATGAAATTTTGCATGGACTGAGTTTGATAATTTTGTGTTAGTGGAATTAACATTGTGTTTATTTAAGA 1200  
AAAAAAATATTTTTTACAGAAACCTACTGAATTTGTAGGGTTTTAAATAACATGATGTCTGGGATTGCTTTTGAAT 1280  
GCTTCAGCCAAAAACAACGAACAACAAAAATAAGGATAGATAAAGCAATGTGACAAAATGCTGATAGTTGTTGGAC 1360  
CTTGGGGAGACACATGCAGAGCCATCACATCACTTTTTTTCAGACATCTTCTTGGTCAGTTATAATCATTTTGTGTTGTC 1440  
CCCACTCCCAATTTCTACTTGCCTCTAGTCCATCCTCCTCACTGCTTGCCAAAGTGATCCTTCTAAACACAAATCTGAT 1520  
CATATTCAAAAAGCTTTTGAAGGGTAAGTTTTATGGTATATGCCATATATCAGTACAACAAACAAATCGTCTGAGGTGC 1600  
CGTTGCCCTACAGGATAAAGTCCAACTCCTTTGCCTGGCACTCCAAGCCCCCACTCTATCTTCTTGGCCTCATCTCTCAT 1680  
GATGTACATCAGCCACATTGCTAGTGTCTGCTCATGGCCTTCTGCCTAGAATGCTTTATGCCCCAGCCAACTATTTACTG 1760  
TCTTCTTCAGTCGACCAGAGTGCAATTTACCTGTTTAAATCTATCATTTTGTATACATTGTGCATGTCTATTATGGCT 1840  
CATATTAAGCAATGCCTTGGATTATAGTAATTTATGTATATGTCTATTTTCATATACTTTAACCTGAACCCCTTCAGAACC 1920  
ATTTCTTTTTCATTTCTTAAGTTCTTTGCACCTAGCCCAGTGCTGGTACGTCGTGGGTATTTCAGTAGATTAAATGCAC 2000  
TTTAAGGAACTTCCCTTGTGTCCATCAAGTGGCTAAGGCTCTGTGCTCCCAATGCAGGGGACCAGGGTTCAATCTCAGG 2080  
TCAGGGAAGTAGATCCACAGGTCACTAAGAGTTTGAAGCCACAACCTACCTGACCTCACATGCCACAACCTAATCGA 2160  
AGATCCCTCGTGTGCACTAAGTCTAGTGCAGTTAAATATATTTTTTAAATGCACCTTTGAATGTGAGAATGAATGATG 2240  
TGTCACAGACACTGTTGTCCCCTGAGAAGGGAGTGAGTAATGATTTGAGGGCCCTCATAGTATATCTTCTTTTATGGAC 2320  
CCAGAGACAGGCACTGGCTTGGTGTCTCAAGGCAGCTCAGAATTAAGCATGGAACAGACAGCTGTATCCAGAGTGGACA 2400  
GAAAGCCAGGGGCTGACTGCTGGAGAGGTAGGAACCTTGGAATTTCCAGGGAGGATATGGTGGAAATGGGTGGGGAGGG 2480  
GAACGGGGTTGAATGTACTTAGGAAGTAGGGAAGGAAAAGGCATACAGGGAGGAGAAGCCAAGGAGCTAATTAATGCAG 2560  
CTGCCCTTTTCAGGTGGCCACATATCCCTGAAGGTGAGCAATGATGGGCTACACTGATTGGGGCAATGCTTCCTTCTC 2640  
TATTGCCTTGCACTTTCTTAAAGCCAAAAGGTGCTGCCAGATGGGCAGGTCTCTGGGCCAACCAACACCATCATCAATG 2720  
GTGAGTACCTCTCCGCTCCTTCCCAAGGTCCAGAATCCCTGGTATCCCCAATGAGCTCAAGGAATCCTCCTCTCTTTT 2800  
TTTTTTTTTTTTTTTACAAATTATATATGTAACACATATTCAGTGCAGAAAATTAGAAAACACAGATAAACCAAAAAGA 2880

Figure 2

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AAAAAATTATAGTTCCCAAATGGGGCACAGAAGACCCAGTGGACATAGAAGTTGGATAGACTTGGATTTAACTGGTT 2960  
ACCAGTATGTGACCTGGACAAGTCACTGAATTGTTTTGTTCTTCCATTCCCTTATCTATAGAATGGGGATGATAACACT 3040  
TTAAAGGTTCTTGTAAGGATTAAAATGTGATAATATATAAGATTTTAGCATAATGCCTGCCCTGTGCTGTGCTTAGTA 3120  
CCTTAGTTTAGACGCTTTGCAACCCCATGGACTGTAGCCACCAGGCTCCTCTGTCCATGTGGATTCTGCAGGCAAGAAT 3200  
ACTGGAGTGGGTACCATGCCTCCTCCAGGGGATCTTCCAACTCAGGGATCGAACCCAGGTCCTAGCCTACAGTATTA 3280  
ATTGATGCTGTTATTTTACTTTTATCCCACTAGCTAGAGCACATCATCCTAGACATTTTGATACATGGCCTACCAATTT 3360  
GTGTCCAGTGTAAGAATATACATGTGTGTGCTCAGTGGCTCAGTCGTGTCTGACTCTTTGCAACCCCATGGACTGTAGCC 3440  
CGCGAAAGCTCCTCTGCCCATGGGATTGCCAGCCAAGAATACTGGAGCAGGTTGCCATTTCTTCTCCAGGGGATCTTT 3520  
CAACACAGGGATTGAATCCTTGTCTCCTGTGTTTCTGCAATTGGCAGGTGTATTCTTTACCCTAGAGCCACTGGGAAAC 3600  
CCCTTAAGTATATACATAAATCTTTATAGTTTCCATTCTCCCTTCTACCCTCCAAATAGGTTATACCAAGGAGAAT 3680  
GTATTTTGGTAGCTAGGCAGTATTCTGAGGCCCTCTCTGGGAGTCATGTTAAAGGTTTGGTGTACAGTGAGGAATGC 3760  
CAGGGATTGAGGGAGACTTGCTGTCTTCTTTTCAGGAGCCAGGTGTGGGGAGGACAGCTGGTATATCCCCAAGAACCTG 3840  
ATGATACCTGCATCTTCCCGATGGGGAGCCCTGCCCTTCTGGCCCTCTATCTCAGAAAAGATGCTTTGTTTATGTCTGG 3920  
AAGACCTGGGGTAAAGATTTCCCTTCTCTGGCCTGTCACTCACACTTAAATCACTTCTTCTACCTGATCCCTTTCTT 4000  
TTGGTCTCATCCTTAAATTCTGTGAGTTTCCCTAATCTTCACTTCCCCCATGACTCCTTCTCTTCCACAGCACCTAGTC 4080  
AACTCTATTATACTTCTTTCTGGGAGCCCTGCTCCAATTATAGTCCCATCCCATGGACCTCTCATAAGGACTTTTCTCC 4160  
TGCCCAACATATGCAAGCTTAAACTCTCTGAAATAACCATCCTTGATACATCTCCTGACCTTCTTCTCTGGTTCCATCT 4240  
CTAACCTGCCCCAGTCTCCTTTGACCAGTAACCCCTTCCCTACTCTTCTTTCCAAAAACCTCAGACCAATACTGGCAA 4320  
GTTCTGGGGGGCCAGTGTCTGGACTGAGCATCGGGACAGACAAGGCAATGCTGGGCACATATAACATGGAAGTGACTGT 4400  
CTACCACCGCCGGGGTCCAGAGCTATGTGCCCCTCGCTCACTCCAGTTCAGCCTTCACTTACTGGTAAGGACTGAG 4480  
GAGGGGACAAGGCCAGTTGACAGGCGAGGAGAAGGTGGGGAGGCTGGGCTGGACAGGAAAGGGGAAAGAGGAATGGTGTG 4560  
TAACCTTACAGGGGCAGAACCAGGAAGATGTGGGCAGAGGGATGTGGGGCTTGGAGCCCGTGAAGGGCCAGGCAGCTTGG 4640  
GTTGGTTGAAAAATATGGCTGTGAAAGAAGAAGCTGACAGAAAGAAGAACTTATGGTTCTCACTTTCTCTGACTCCAATC 4720  
CCAGACCAGGTGCCCTTCTCTGTGAGTGTGTCTCAGCTGCAGGCCTTGGATGGAAGGAACAAGCGCTTCTTGAGAAAGCA 4800  
GCCTCTGACCTTTGCCCTCCAGCTCCATGATCCCACTGGCTATTGCGCTGGGGCTGACCTTTCTTACCTGGGACTTTG 4880  
GTGACAGTACAGGGACCTGATCTCTCGGGCACTCAGGTCACACTTACCTAGAGTCTGGCCCACTCACTGCACAG 4960  
GTGGTGTGTCAGGCTGCCATTCTCTCACCTCCTGTGGCTCCTCTCCAGTTCAGGCACCTACAGATAGGCATGTGACAAC 5040  
TGCAGAGGCTCCTGGAACCACAGCTGGCCAAGTGCCTACTACAGAAGTCATGGGCACCACCTGGCCAGGTGCCAACTG 5120  
CAGAGGCCCTGGCACCACAGTTGGGTGGGTGCCAACCCAGAGGATGTAGGTACCACACCTGAGCAGGTGGCAACCTCC 5200  
AAAGTCTTAAGTACAACACCAGTGGAGATGCCAACTGCAAAAGCTACAGGTAGGACACCTGAAGTGTCAACTACAGAGCC 5280  
CTCTGGAACCACAGTTACACAGGGAACAACCTCCAGAGCTGGTGGAGACCACAGCTGGAGAGGTGTCCACTCCTGAGCCTG 5360  
CGGGTTCAAATACTAGCTCATTCATGCCTACAGAAGGTACTGCAGGTAAGGGGGCCACCATGAATGAGTTCATAGAGGTG 5440  
GGGCATTTGTACAGCTCTGAAGACCTGAAAGAATTGCTCAGGACCCAGATGTTACTCAATCCTTAGCTTAGCAGTGGAG 5520  
TCCCTCAGAATCTTCACTGGTTTTAAACCCCTTAAGTCCCTCTTAATGGCACAGAATAGATCCAGAGTTCAGGAAACC 5600  
AGGGTCTTCTCCTAGGCCAGGGTAGAGAGCTTATCTCTCTTCTGAGAGAAGTTCAGGAAGCAGTGTGTGATCATTT 5680  
GGTGGTGGTGTCTCAGTCATGTCTGACTCTTTGTGACCTCATGGACTATGGCCACCAGGCTCCTCTGTCCATAGAATTCT 5760

Figure 2 (continued 1)

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CCAGGCAAGAACACTGGAGTGGGTGGCCATTTCTTCTCCAGGGGATTTCCCTGCCAGGGATTAAACCCGAATTGGCA 5840  
GGTGGATTCTTTACCCGAGCCACCTAGAAAGTCCCATTGTGATCATTAGATAATACTTATACCTCATTTTCTGATTAAGTG 5920  
TAAACACAGAAATCTTTCTGACACCACTTCCCACCCCTGGATTCCCATCCCAAAGTAGGTTTACCTGGAATTGTGGTAGG 6000  
AATACTAAAAAGGGAGAAGTGAGATAGTGACACTATGACTTAACACATGTCAAATGTCTGACCCAGGACCTGGCACAGTG 6080  
TAGGGTGTGATAAACATTTGGGATGTCTAAAATTCTGACTCTAACCTGTGACTCTGGGGCAGTCATTTCTCTTGGGCCT 6160  
TTCTTTATCTTAAAAATGAGAGTTTCCAGCTCTTGTCTGATTCTAAGCCTGGATCCAGTAGCTCTGACTCTACCTGGAA 6240  
AAATGCTTGTGGGCCTGTTTTTCAGGTTAGTCATTTGCTTTTTGACTTTGCCTCTTTAATCCTCTCCTCCAGGCTCCCTG 6320  
AGTCCCCTGCCGGATGACACTGCCACCTTAGTCTGGAGAAGCGCCAAAGCCCCCTGGATTGTGTCTGTATCGCTATGG 6400  
CTCCTTTTCCCTCACCCTGGACATTGTCCGTGAGTCTTGCCCTACATTGTCCGTAAGCTGGTGGAGGGAGCGTGTGCTGC 6480  
TTAGGGTTGCCCAGTGGAAGCACACCTTGAAGGAATTACTCACCTGGACAAGGAGAATACCCAGATCCCAGGGGTTTCA 6560  
TATGAAGGCAGAAATGGGATTAGGGAGGCAGCCCGAGGACCTTCTGGCCATGGGCCTTGGGGGAGGATAAGTAGAGGAGT 6640  
CTCAGACTTAAAAAATCTTGCAACTTTGCAGAGGGTATTGAGAGTGCTGAGATCCTACAGGCTGTGTCTATCCAGTGAAG 6720  
GAGATGCATTTGAGCTGACTGTGTCTTGCCAAGGCGGGTGAGTGTCCACGGTTGCCCTGAGAACTCCTGGGGTGACTGC 6800  
TGTCTGTCTCTGGTGTCTAGTGTCCCTTCCCAGATTCCCTGACGTAAGCTGACATCTCTCCCAGGCTACCCAAGGAAG 6880  
CCTGCTGACATCTCATCGCCAGGGTGTGAGCTGCCTGCCAGCGCTGTGTGAGCCTGTGCCCCCAGCCAGCCTGC 6960  
CAGCTGGTTTTGCACCAGGTACTGAAGGGTGGCTCAGGGACCTACTGCCTCAATGTGTCTTTGGCTGATGCCAATAGCCT 7040  
GGCGATGGTCAGACCCAGCTTGTGTCATGCTGGTAGGTAGTTGGACAAGAGGTAGGATGAAGACACGGGGAGATGGTAGA 7120  
GGTTACCTACTAGAGGAAGCAGACACTGAATGCAGCCGTATCTGGGATTCCACCCATAGGGCAAGAAGCAGGCCTCAGGC 7200  
AGGCTCCTCTGTCTGTTGGGCATCTTGTGCTGCTAACAGCTTTGTGCTTGCTGATCTCTGATATACAGGTGAGATCCCCGC 7280  
CATCCTGCTCCCACTCCTTTACCCCTTATTACCACCACCACTCTTCTCATGGGAAGAAGAAACCACCAACCCCTTTGGG 7360  
AAAGTGTAGAGTCCAAGAAAGAGCCAGACTTGGGAAGTTCAACAGGTCTAGGCTGCAGTCTTGTCTGGTGGGACCTGGGG 7440  
AAGTCCATTAAACCTTCTGAGCCACTGAAAAGTAGGAAACATAATACCTGTCTGTGGGGCTGTTTTTCAGGGCTCTAGAC 7520  
AATGTGAGTAAACACCTGGTTCTGAAACAAAAGTGAATAAATGATGATCTCAATGACTGTTGTTATGAATAATATCAA 7600  
CAGTGGAGAAGAACTCAGTGAAGTCTTCCACCTGCCAGAAAGGCAATCCCTAGGCCTGGAGGGCTGAGGTCTCTCA 7680  
AAGCAGGGAAGCCTGTAGGGTGAAGGGAAATGGTCAGAGCTTACCATAAACATAAGAGAGGATAAACCCCTGTTGGTGAG 7760  
AAGAGGAGGGAGCCAGGATCAAGACCAAGTCAACCTGGGTTATGGTTTAGTCTTTTTTTTTTAGAGAAGCACAAAGAGGT 7840  
TGCCATTGACCACCACTAACCAGTATCCCTGCTTTTCTCCCAATATCAGGCGAAGACTTATGAAGCAAGGCTCAGCAGTC 7920  
CCCCCTCCCAGCTGCCACACGGTAGAACCCAGTGGCTACGTCTGCCCTGGGTCTTCCGCTCTTGCCCCATTGGTGAGAG 8000  
CAAACCCCTCCTCAGTGGACAGCAGGTCTGAGTGCTCTTATGTGAAGTCATGATTACCCAGGTGGACAGCAAGGCCTGT 8080  
CTTTTCTCTGGTCTTCCCTCAGAGACTACCATTGCCTGAAATAAAGACTCAGAACTTG 8138

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Figure 2 (continued 2)

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cDNA CH	GGTCTTTGGTTGCTGGAAGGAAGAACAGGATGGATCTGGTGCTGAGAAAATACCTTCTCC	60
cDNA RPE1	-----	
cDNA CH	ATGTGGCTCTGATGGGTGTTCTTCTGGCTGTAAGGACCACAGAAGGACCCAGAGACAGGG	120
cDNA RPE1	-----	
cDNA CH	ACTGGCTTGGTGCTCAAGGCAGCTCAGAATTAAAGCATGGAACAGACAGCTGTATCCAG	180
cDNA RPE1	-----	
cDNA CH	AGTGGACAGAAAGCCAGGGCCTGACTGCTGGAGAGGTGGCCACATATCCCTGAAGGTCA	240
cDNA RPE1	-----	
cDNA CH	GCAATGATGGGCCTACACTGATTGGGGCAAATGCTTCCTTCTCTATTGCCTTGCACTTTC	300
cDNA RPE1	-----	
cDNA CH	CTAAAGCCAAAAGGTGCTGCCAGATGGGCAGGTCATCTGGGCCAACAACACCATCATCA	360
cDNA RPE1	-----	
cDNA CH	ATGGGAGCCAGGTGTGGGGAGGACAGCTGGTATATCCCCAAGAACCTGATGATACCTGCA	420
cDNA RPE1	-----	
cDNA CH	TCTTCCCCGATGGGGAGCCCTGCCCTTCTGGCCCTCTATCTCAGAAAAGATGCTTTGTTT	480
cDNA RPE1	-----	
cDNA CH	ATGTCTGGAAGACCTGGGACCAATACTGGCAAGTTCTGGGGGGCCAGTGTCTGGACTGA	540
cDNA RPE1	-----CCAACTACTGGCAAGTTCTGGGGGGCCAGTGTCTGGACTGA	41
	*****	
cDNA CH	GCATCGGGACAGACAAGGCAATGCTGGGCACATATAACATGGAAGTGACTGTCTACCACC	600
cDNA RPE1	GCATCGGGACAGACAAGGCAATGCTGGGCACATATAACATGGAAGTGACTGTCTACCACC	101
	*****	
cDNA CH	GCCGGGGGTCCCAGAGCTATGTGCCCCTCGCTCACTCCAGTTCAGCCTTCACCATTACTG	660
cDNA RPE1	GCCGGGGGTCCCAGAGCTATGTGCCCCTCGCTCACTCCAGTTCAGCCTTCACCATTACTG	161
	*****	
cDNA CH	ACCAGGTGCCCTTCTCTGTGAGTGTGTCTCAGCTGCAGGCCTTGGATGGAAGGAACAAGC	720
cDNA RPE1	ACCAGGTGCCCTTCTCTGTGAGTGTGTCTCAGCTGCAGGCCTTGGATGGAAGGAACAAGC	221
	*****	
cDNA CH	GCTTCCTGAGAAAGCAGCCTCTGACCTTTGCCCTCCAGCTCCATGATCCCAGTGGCTATT	780
cDNA RPE1	GCTTCCTGAGAAAGCAGCCTCTGACCTTTGCCCTCCAGCTCCATGATCCCAGTGGCTATT	281
	*****	
cDNA CH	TGGCTGGGGCTGACCTTTCCTACACCTGGGACTTTGGTGACAGTACAGGGACCCTGATCT	840
cDNA RPE1	TGGCTGGGGCTGACCTTTCCTACACCTGGGACTTTGGTGACAGTACAGGGACCCTGATCT	341
	*****	
cDNA CH	CTCGGGCACTCACGGTCACTCACACTTACCTAGAGTCTGGCCCAGTCACTGCACAGGTGG	900
cDNA RPE1	CTCGGGCACTCACGGTCACTCACACTTACCTAGAGTCTGGCCCAGTCACTGCACAGGTGG	401
	*****	
cDNA CH	TGCTGCAGGCTGCCATTTCCTCTCACCTCCTGTGGCTCCTCTCCAGTTCCAGGCACTACAG	960
cDNA RPE1	TGCTGCAGGCTGCCATTTCCTCTCACCTCCTGTGGCTCCTCTCCAGTTCCAGGCACTACAG	461
	*****	

Figure 3

TITLE: USE OF SILVER GENE FOR THE AUTHENTICATION OF THE RACIAL ORIGIN OF ANIMAL POPULATIONS, AND OF THE DERIVATIVE PRODUCTS THEREOF

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cDNA CH	ATAGGCATGTGACAACCTGCAGAGGCTCCTGGAACCACAGCTGGCCAAGTGCCTACTACAG	1020
cDNA RPE1	ATAGGCATGTGACAACCTGCAGAGGCTCCTGGAACCACAGCTGGCCAAGTGCCTACTACAG	521
*****		
cDNA CH	AAGTCATGGGCACCAACACCTGGCCAGGTGCCAACTGCAGAGGCCCTGGCACCACAGTTG	1080
cDNA RPE1	AAGTCATGGGCACCAACACCTGGCCAGGTGCCAACTGCAGAGGCCCTGGCACCACAGTTG	581
*****		
cDNA CH	GGTGGGTGCCAACCACAGAGGATGTAGGTACCACACCTGAGCAGGTGGCAACCTCCAAAG	1140
cDNA RPE1	GGTGGGTGCCAACCACAGAGGATGTAGGTACCACACCTGAGCAGGTGGCAACCTCCAAAG	641
*****		
cDNA CH	TCTTAAGTACAACACCACTGGAGATGCCAACTGCAAAAGCTACAGGTAGGACACCTGAAG	1200
cDNA RPE1	TCTTAAGTACCACACCACTGGAGATGCCAACTGCAAAAGCTACAGGTAGGACACCTGAAG	701
*****		
cDNA CH	TGTCAACTACAGAGCCCTCTGGAACCACAGTTACACAGGGAACAACCTCCAGAGCTGGTGG	1260
cDNA RPE1	TGTCAACTACAGAGCCCTCTGGAACCACAGTTACACAGGGAACAACCTCCAGAGCTGGTGG	761
*****		
cDNA CH	AGACCACAGCTGGAGAGGTGTCCACTCCTGAGCCTGCGGGTTCAAATACTAGCTCATTC	1320
cDNA RPE1	AGACCACAGCTGGAGAGGTGTCCACTCCTGAGCCTGCGGGTTCAAATACTAGCTCATTC	821
*****		
cDNA CH	TGCCTACAGAAGGTACTGCAGGCTCCCTGAGTCCCCTGCCGGATGACACTGCCACCTTAG	1380
cDNA RPE1	TGCCTACAGAAGGTACTGCAGGCTCCCTGAGTCCCCTGCCGGATGACACTGCCACCTTAG	881
*****		
cDNA CH	TCCTGGAGAAGCGCCAAGCCCCCTGGATTGTGTTCTGTATCGCTATGGCTCCTTTTCCC	1440
cDNA RPE1	TCCTGGAGAAGCGCCAAGCCCCCTGGATTGTGTTCTGTATCGCTATGGCTCCTTTTCCC	941
*****		
cDNA CH	TCACCCTGGACATTGTCCAGGGTATTGAGAGTGCTGAGATCCTACAGGCTGTGTATCCA	1500
cDNA RPE1	TCACCCTGGACATTGTCCAGGGTATTGAGAGTGCTGAGATCCTACAGGCTGTGTATCCA	998
*****		
cDNA CH	GTGAAGGAGATGCATTTGAGCTGACTGTGTCTTGCCAAGGCGGGCTACCCAAGGAAGCCT	1560
cDNA RPE1	GTGAAGGAGATGCATTTGAGCTGACTGTGTCTTGCCAAGGCGGGCTACCCAAGGAAGCCT	1058
*****		
cDNA CH	GCATGGACATCTCATCGCCAGGGTGTGCTGCTGCCTGCCAGCGGCTGTGTGCTGCTGTC	1620
cDNA RPE1	GCATGGACATCTCATCGCCAGGGTGTGCTGCTGCCTGCCAGCGGCTGTGTGCTGCTGTC	1118
*****		
cDNA CH	CCCCAGCCCAGCCTGCCAGCTGGTTTTGCACCAGGTACTGAAGGGTGGCTCAGGGACCT	1680
cDNA RPE1	CCCCAGCCCAGCCTGCCAGCTGGTTTTGCACCAGGTACTGAAGGGTGGCTCAGGGACCT	1178
*****		
cDNA CH	ACTGCCTCAATGTGTCTTTGGCTGATGCCAATAGCCTGGCGATGGTCAGCACCCAGCTTG	1740
cDNA RPE1	ACTGCCTCAATGTGTCTTTGGCTGATGCCAATAGCCTGGCGATGGTCAGCACCCAGCTTG	1238
*****		
cDNA CH	TCATGCCTGGGCAAGAAGCAGGCCTCAGGCAGGCTCCTCTGTTCGTGGGCATCTTGCTGG	1800
cDNA RPE1	TCATGCCTGGGCAAGAAGCAGGCCTCAGGCAGGCTCCTCTGTTCGTGGGCATCTTGCTGG	1298
*****		
cDNA CH	TGCTAACAGCTTTGTTGCTTGCTGCTGCTGATATACAGGCGAAGACTTATGAAGCAAGGCT	1860
cDNA RPE1	TGCTAACAGCTTTGTTGCTTGCTGCTGCTGATATACAGGCGAAGACTTATGAAGCAAGGCT	1358
*****		
cDNA CH	CAGCAGTCCCCCTTCCCCAGCTGCCACACGGTAGAACCCAGTGGCTACGTCTGCCCTGGG	1920
cDNA RPE1	CAGAAGTCCCCCTTCCCCAGCTGCCACACGGTAGAACCCAGTGGCTACGTCTGCCCTGGG	1418
*** *****		

Figure 3 (continued 1)

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cDNA CH      TCTTCCGCTCTTGCCCCATTGGTGAGAGCAAACCCCTCCTCAGTGGACAGCAGGTCTGAG 1980
cDNA RPE1    TCTTCCGCTCTTGCCCCATTGGTGAGAGCAAACCCCTCCTCAGTGGACAGCAGGTCTGAG 1478
*****

cDNA CH      TGCTCTTATGTGAAGTCATGATTTACCCAGGTGGACAGCAAGGCCTGTCTTTTCTCTGGT 2040
cDNA RPE1    TGCTCTTATGTGAAGTCATGATTTACCCAGGTGGACAGCAAGGCCTGTCTTTTCTCTGGT 1538
*****

cDNA CH      CTTCCCTCAGAGACTACCATTGCCTGAAATAAAGACTCAGAACTTG 2086
cDNA RPE1    CTTCCCTCAGAGACTACCATTGCCTGAAATAAAGACTCAGAACTTG 1584
*****
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Figure 3 (continued 2)



TITLE: USE OF SILVER GENE FOR THE AUTHENTICATION OF THE RACIAL ORIGIN OF ANIMAL POPULATIONS, AND OF THE DERIVATIVE PRODUCTS THEREOF

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Prot. CH      MDLVLRKYLHVALMGVLLAVRTTEGPRDRDWLGVSRLRIKAWNRLYPEWTESQGPDC 60
Prot. RPE1    -----

Prot. CH      WRGGHISLKVSNDGPTLIGANASFISIALHFPKSKQVLPDQGVITWANNTIINGSQVWGGQL 120
Prot. RPE1    -----

Prot. CH      VYPQEPDDTCIFPDGEPSPGSLSQKRCFVYVWKTWDQYWQVLGGPVSGLSIGTDKAMLG 180
Prot. RPE1    -----QYWQVLGGPVSGLSIGTDKAMLG 23
                  *****

Prot. CH      TYNMEVTVYHRRGSQSIVPLAHSSSAFTITDQVPFSVSVSQLQALDGRNKRFLRKQPLTF 240
Prot. RPE1    TYNMEVTVYHRRGSQSIVPLAHSSSAFTITDQVPFSVSVSQLQALDGRNKRFLRKQPLTF 83
                  *****

Prot. CH      ALQLHDPGSGYLAGADLSYTWDFGDSTGTLSRALTVTHTYLES GPVTAQVVLQAAIPLTS 300
Prot. RPE1    ALQLHDPGSGYLAGADLSYTWDFGDSTGTLSRALTVTHTYLES GPVTAQVVLQAAIPLTS 143
                  *****

Prot. CH      CGSSPVPGTDDRHTTAEAPGTTAGQVPTTEVMGTTPGQVPTAEAPGTTVGWVPTTEDVG 360
Prot. RPE1    CGSSPVPGTDDRHTTAEAPGTTAGQVPTTEVMGTTPGQVPTAEAPGTTVGWVPTTEDVG 203
                  *****

Prot. CH      TTPEQVATSKVLSTTPVEMPTAKATGRTPEVSTTEPSGTTVTQGTTPELVETTAGEVSTP 420
Prot. RPE1    TTPEQVATSKVLSTTPVEMPTAKATGRTPEVSTTEPSGTTVTQGTTPELVETTAGEVSTP 263
                  *****

Prot. CH      EPAGSNTSSFMPTEGTAGSLSPDPDDTATLVLEKRAPLDCVLYRGSFSLTLDIVQIE 480
Prot. RPE1    EPAGSNTSSFMPTEGTAGSLSPDPDDTATLVLEKRAPLDCVLYRGSFSLTLDIV-SIE 322
                  *****

Prot. CH      SAEILQAVSSSEGDAFELTVSCQGGPLKEACMDISSPGCQLPAQRLCQFVPPSPACQLVL 540
Prot. RPE1    SAEILQAVSSSEGDAFELTVSCQGGPLKEACMDISSPGCQLPAQRLCQFVPPSPACQLVL 382
                  *****

Prot. CH      HQVLKGGSGTYCLNVSLADANSLAMVSTQLVMPGQEAQRLQAPLFVGILLVLTALLLASL 600
Prot. RPE1    HQVLKGGSGTYCLNVSLADANSLAMVSTQLVMPGQEAQRLQAPLFVGILLVLTALLLASL 442
                  *****

Prot. CH      IYRRRLMKQGSVAVPLPQLPHGRTQWLRLPWVFRSCPIGESKPLLGGQV 649
Prot. RPE1    IYRRRLMKQGSVAVPLPQLPHGRTQWLRLPWVFRSCPIGESKPLLGGQV 491
                  *****
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Figure 4